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BVB Campus, Vidyanagar, Hubballi – 580031, Karnataka, INDIA.

SCHOOL OF COMPUTER SCIENCE AND ENGINEERING

Project report on

BRAIN TUMOR DETECTION AND CLASSIFICATION USING DEEP LEARNING MODELS

Submitted

in partial fulfillment of the requirements for the award of the degree of

Bachelor of Engineering

in

COMPUTER SCIENCE AND ENGINEERING

Submitted By

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SCHOOL OF COMPUTER SCIENCE AND ENGINEERING

KLE Technological University, Hubballi

2023-2024

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2023-24

CERTIFICATE

This is to certify that project entitled "Brain Tumor Detection and Classification using Deep Learning Models" is a bonafied work carried out by the student team Manjunath Pujar - 01FE21BCS417, H Kavanashree - 01FE20BCS236, Jithendra M - 01FE21BCS429, Shankaraling Halemani - 01FE20BCS170, in partial fulfillment of the completion of 7th semester B. E. course during the year 2023 – 2024. The project report has been approved as it satisfies the academic requirement with respect to the project work prescribed for the above said course

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ABSTRACT

Brain tumors represent a significant health concern globally, contributing to a high mortality rate. Timely detection and intervention are critical for improving patient outcomes. This study proposes an intelligent model for brain tumor prediction using MRI images, leveraging advanced deep learning algorithms. The system comprises key stages, including data collection, preprocessing, feature extraction, and prediction. Six distinct models - AlexNet, VGG16, ResNet-50, GoogleNet, Xception and DenseNet-121 were evaluated for their performance. The results show that the DenseNet-121 outperformed others with an accuracy of 98.10%. This proposed system offers a reliable and efficient approach to predict brain tumor likelihood, serving as a valuable screening tool for early detection. The user-friendly design, tailored for medical professionals, includes an intuitive interface for inputting patient data and receiving prediction results. The system holds the potential to enhance survival rates and mitigate the mortality associated with brain tumors, providing doctors with an effective tool for early disease detection.

Keywords :*Data preprocessing, MRI images, Deep Learning models.*

ACKNOWLEDGEMENT

The satisfaction and euphoria that accompany the successful completion of any task would be incomplete without the mention of a number of individuals whose professional guidance and encouragement helped me in the successful completion of this report work.

We take this opportunity to thank Dr. Ashok Shettar, Vice-Chancellor and to Dr. Basavaraj Anami, Registrar, KLE Technological University, Hubballi.

We also take this opportunity to thank Dr. Vijaylakshmi M, Professor and Head of School, School of Computer Science and Engineering for having provided us academic environment which nurtured our practical skills contributing to the success of our project.

We sincerely thank our guide Prof. Vidya Handur, Associate Professor, School of Computer Science and Engineering for her guidance, inspiration and wholehearted co-operation during the course of completion.

We sincerely thank our project co-ordinator Ms Priyadarshini Patil for her support, motivation and wholehearted co-operation during the course of completion.

Our gratitude will not be complete without thanking the Almighty, our beloved Parents, our seniors and our friends who have been a constant source of blessings and inspiration.

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Chapter 1

INTRODUCTION

Brain tumors are cellular growths in or around the brain that can affect surrounding structures like nerves, the pituitary gland, the pineal gland, and brain membranes as well as brain tissue. When cancer spreads from other regions of the body to the brain, it can cause secondary, or metastatic, brain tumors that start in the brain. In the United States, a primary brain tumor is identified in just 5 out of every 100,000 persons annually[1]. In the US, a brain or central nervous system tumor is identified in about 4,100 children under the age of 15.

Brain tumors can take many different forms. The kind of cells that make up the tumor determine the type of brain tumor. On the tumor cells, specialized lab tests can reveal information about the cells. This data is used by your medical team to identify the kind of brain tumor[2]. In the brain tissue, gliomas—growths of glial cell-like cells—surround and support nerve cells. They can be benign or cancerous, the most prevalent variety being glioblastoma. Cerebrospinal fluid-derived choroid plexus tumors can either be benign or malignant. Malignant embryonal tumors commonly affect infants and young children. The majority of benign germ cell tumors, which develop from germ cells, affect children more frequently than adults. Pineal tumors have the potential to be either benign or cancerous. Other forms of brain tumors include meningiomas, nerve tumors, and pituitary tumors. Muscles, blood arteries, connective tissue, and the skull's bones can all develop uncommon tumors. Virus-fighting immune system cells in the brain can give rise to malignant brain tumors.

Most brain tumors of certain forms are not malignant. These are referred to as benign or noncancerous brain tumors, which can grow slowly and push on brain tissue. Most brain tumors of certain forms are malignant. These are referred to as malignant brain tumors or brain cancers, which can grow swiftly, penetrate, and kill brain tissue. Both benign and malignant brain tumor kinds exist. Brain tumors that are benign typically grow slowly. Fast-growing brain tumors are frequently those that are malignant. Brain tumors can be extremely small or very large, with some being discovered when symptoms are apparent and others growing huge before being discovered. Treatment options for brain tumors depend on the type, size, and location of the tumor, with common treatments including surgery and radiation therapy.

Unfortunately, the symptoms of brain tumors often overlap with other neurological conditions, making early diagnosis challenging. This is where the need for specialized detection models becomes evident. These models can identify even subtle abnormalities that might be missed by the human eye, helping healthcare providers make timely and accurate diagnoses.

These models have the power to bridge healthcare disparities and ensure that individuals across the globe have a fighting chance against the danger posed by brain tumors. In essence, the development of brain tumor detection models isn't just a technological advancement; it's a humanitarian endeavor that promises to improve outcomes and save lives for those facing the ominous reality of brain tumors.

1.1 Motivation

The imperative to develop a deep learning model for brain tumor detection and classification is underscored by the formidable challenges posed by these potentially fatal conditions. Brain tumors exhibit variations in size, location, and type, intensifying the complexity of their detection. Early identification is pivotal for effective treatment, prompting the exploration of advanced computational models, such as deep learning, as rapid processors of large medical imaging datasets. The accelerated analysis offered by these deep learning models significantly reduces patient waiting times for critical results, providing a crucial advantage in urgent medical scenarios. These advanced computational tools empower radiologists and neurologists to make more informed decisions, elevating the quality of patient care. The motivation to refine and enhance deep learning models stems from the quest to improve prediction accuracy, ensuring more reliable and precise diagnoses. As an integral part of ongoing medical advancements, research in brain tumor detection and classification not only strives to enhance immediate patient outcomes but also contributes to transformative progress in the fields of neurology and radiology.

1.2 Literature Review / Survey

This article [3] presents a study on brain tumor detection using the VGG-16 model, a convolutional neural network known for its performance in computer vision tasks. The aim of the study is to classify magnetic resonance imaging (MRI) images and accurately identify the presence of brain tumors. The dataset used consists of brain tumor MRI images, categorized into two classes: "NO" (no tumor) and "YES" (tumor). The methodology involves setting up the environment, importing and preprocessing the data, building the VGG-16 model, and evaluating its performance using metrics such as accuracy, precision, and recall. The results demonstrate an accuracy of approximately 88% on the validation set and 80% on the test set, indicating the potential of the VGG-16 model in supporting healthcare professionals in diagnosing brain tumors.

This work [4] presents an automatic technique for brain tumour classification from MRI data, wherein image slice samples are fed into a Convolutional Neural Network (CNN)-based Squeeze and Excitation ResNet model. Without data augmentation, experimental evaluation reveals that the suggested CNN archives an overall accuracy rate of 89.93%. With an overall accuracy of 93.83%, the addition of data augmentation has further increased the accuracies up to 98.67%, 91.81%, and 91.03% for pituitary tumour, meningioma, and glioma, respectively.

This article presents a convolutional neural network based on complex networks (CNNBCN) with a modified activation function for the classification of brain tumours using magnetic resonance imaging [5]. The network structure is produced via randomly generated graph algorithms rather than being manually developed and optimised. The improved CNNBCN model achieves 95.49% classification accuracy for brain tumours. Furthermore, in the studies, the modified CNNBCN model's test loss for brain tumour classification is less than that of the ResNet, DenseNet, and MobileNet models.

This paper proposes a convolutional neural network (CNN) architecture for the effective use of MR images in brain tumour diagnosis. The total size of the dataset is 3264 MR images, which are further subdivided into 4 types: glioma tumour (926 photographs), pituitary tumour (900 images), meningioma (937 photos), and no tumour (500 images). In addition, this article [6] compares the suggested architecture with a number of models, including ResNet-50, VGG16, and Inception V3. An accuracy of 93.3% was found for the CNN model using a dataset of 3264 MR images.

The use of radiography pictures in medical diagnosis is essential, and the development of machine learning (ML) and artificial intelligence (AI) methods has greatly automated the detection of diseases. This study [7] employs a customised pre-trained deep neural network, DenseNet201, to automate the detection and categorization of brain tumours from Magnetic Resonance Images (MRI). Seventy-two MRI pictures from four different classes—notumor, glioma, meningioma, and pituitary—make up the dataset. With 91% training accuracy and 88% testing accuracy, the model performed well. The article suggests a hybrid approach that combines machine learning and deep learning techniques to increase tumour classification and feature extraction even further. The study emphasises the necessity to incorporate a wider range of tumour forms that are common in Indian populations, addressing approximately 150 recorded brain tumour kinds, for a more thorough and efficient automation approach, even if the existing dataset only covers four tumour classes.

To improve tumour identification, a number of image-processing-based computer-aided diagnostic methods have been developed. In these methods, segmentation and classification are crucial phases. To differentiate healthy brain tissue from tumour tissue in MRI images, segmentation techniques such as pixel classification, region-based approaches, and thresholding are used. The goal of classification methods like artificial neural networks and support vector machines is to distinguish between brain images that show tumours and those that do not. A method for preprocessing brain MRI pictures, segmenting them using the k-means clustering algorithm, and extracting texture characteristics using the grey level co-occurrence matrix is presented in this study [8]. A support vector machine is trained for classification using these features. With an impressive accuracy score of 95.21%, this model shows efficacy on par with other models that have been proposed in the literature, highlighting its potential as a reliable tool for brain tumour identification.

1.3 Problem Statement

The brain tumor detection is challenging due to the need of early and accurate detection. Identifying them early is crucial for effective treatment. The existing methods are slow and causing delay in patient care. Hence there is need to develop methods to enhance the detection of brain tumors in the medical images. With advancement in AI models,the deep learning models can be employed to quickly analyse medical images that can significantly reduce wait time of patients and improve decision making. Given the MRI brain tumor medical images the task is to automate the predication and classification of images using deep learning models.

1.4 Problem Analysis

1.4.1 Design Principles

The design principles suitable for identified problem statement in designing solution are :

MVC Model

- MVC separates the system into Model (tumor detection logic), View (user interface), and Controller (user interaction) for clear code organization and easier maintenance.
- It allows components to be modified or extended independently, making it ideal for evolving medical applications with changing tumor detection algorithms.
- MVC streamlines testing and debugging, ensuring system reliability, which is crucial for medical applications.
- It enables flexible user interface design, accommodating different user needs, devices, and platforms for an optimal user experience.

User Experience design (UX)

- UX design centers on user needs, resulting in a user-friendly and efficient system tailored to healthcare professionals' requirements.
- UX design excels at creating clear data displays, simplifying the interpretation of complex medical information for radiologists and doctors.
- UX design ensures an intuitive interface for users with varying expertise, enhancing efficiency, reducing errors, and promoting accessibility for all users.

1.4.2 Scope and Constraints

- The system predicts four types of brain tumor.
- The system takes Magnetic Resonance Imaging (MRI) data.

1.5 Objectives

- To design and develop a user interactive web application for model interaction.
- To analyze and Pre process the data.
- To measure the accuracy of various models.

Chapter 2

REQUIREMENT ANALYSIS

2.1 Functional Requirements

- The system shall accept MRI images as input.
- The system shall be able to classify brain tumors into relevant categories, such as glioma, no tumor, meningioma and pitutary tumor.
- User shall be able to login into the web application.
- User shall be able to view the results.
- The system shall provide clear and interpretable results, including classification labels.

2.2 Non Functional Requirements

- The model shall predict and classify the input image within 5 seconds.
- The system shall be able to process user request within 10 seconds.

2.3 Hardware Requirements

- CPU intel core i3.
- RAM 8GB.
- GPU intel
- Storage SSD or HDD, minimum free space of 1GB.

2.4 Software Requirements

- Reactjs Library
- OpenCV
- Django Framework
- MySQL
- Tensorflow

Chapter 3

SYSTEM DESIGN

System design, a critical phase in software development, involves planning the architecture, components, and interfaces of a software system. It serves as a detailed blueprint, guiding developers in constructing the software to meet specified requirements efficiently.
This section discuss about various design principles and system architecture that is suitable for the project.

3.1 Architectural Framework/System Design

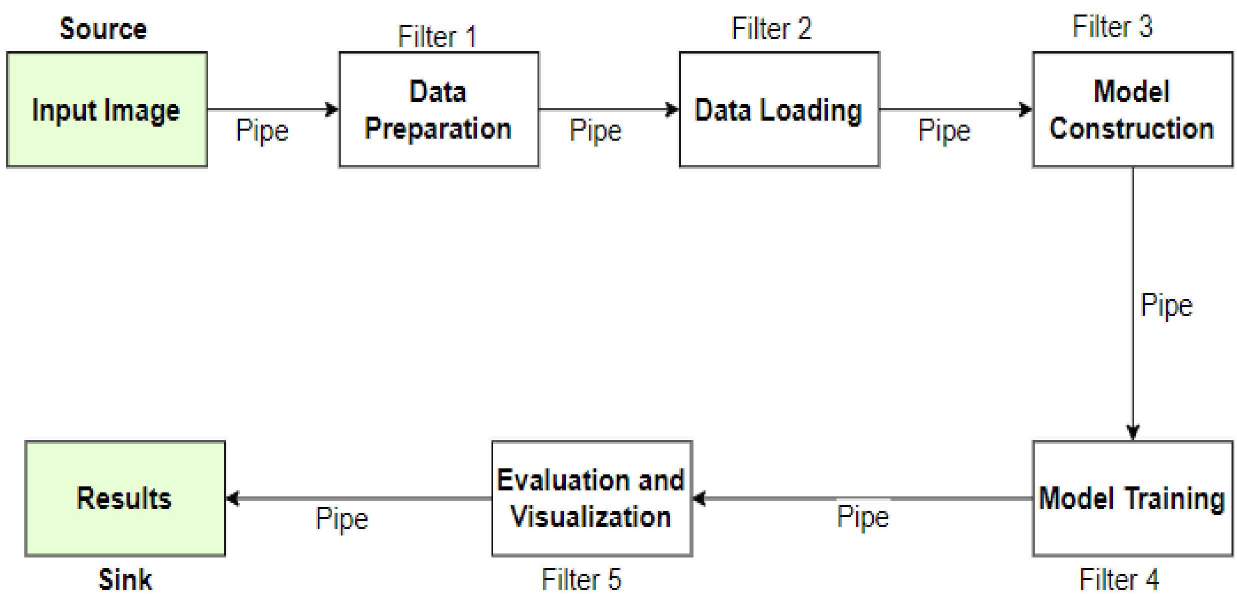

Figure 3.1: Pipe and Filter architecture

1. Data Preparation (Filter 1):
    - Defines key data-related parameters, such as data directories, image dimensions, and augmentation settings.
    - This source filter provides the initial configuration needed for subsequent processing stages.
2. Data Loading (Filter 2):
    - Loads and preprocesses the data using an ImageDataGenerator or similar technique.
    - The filter reads the raw data, applies preprocessing steps (e.g., normalization, augmentation), and prepares it for model training.
3. Model Construction (Filter 3):
    - Constructs the neural network architecture for brain tumor classification.
    - This filter defines the layers, architecture, and parameters of the deep learning model.
4. Model Training (Filter 4):
    - Trains the constructed model using training and validation datasets.
    - The filter takes the prepared data and the constructed model, then performs the training process, optimizing the model's parameters.
5. Evaluation and Visualization (Filter 5):
    - Evaluates the trained model on a separate test set and creates visualizations for analysis.
    - This filter calculates metrics (e.g., accuracy, loss) on the test set, and creates visualizations such as accuracy/loss plots and confusion matrices to assess the model's performance.
6. Results (Sink Filter):
    - Saves the trained model, visualization plots, and evaluation results to files.
    - The sink filter is responsible for persisting the trained model to disk, saving visualizations, and logging evaluation results.

3.2 Design Principles

3.2.1 MVC Model

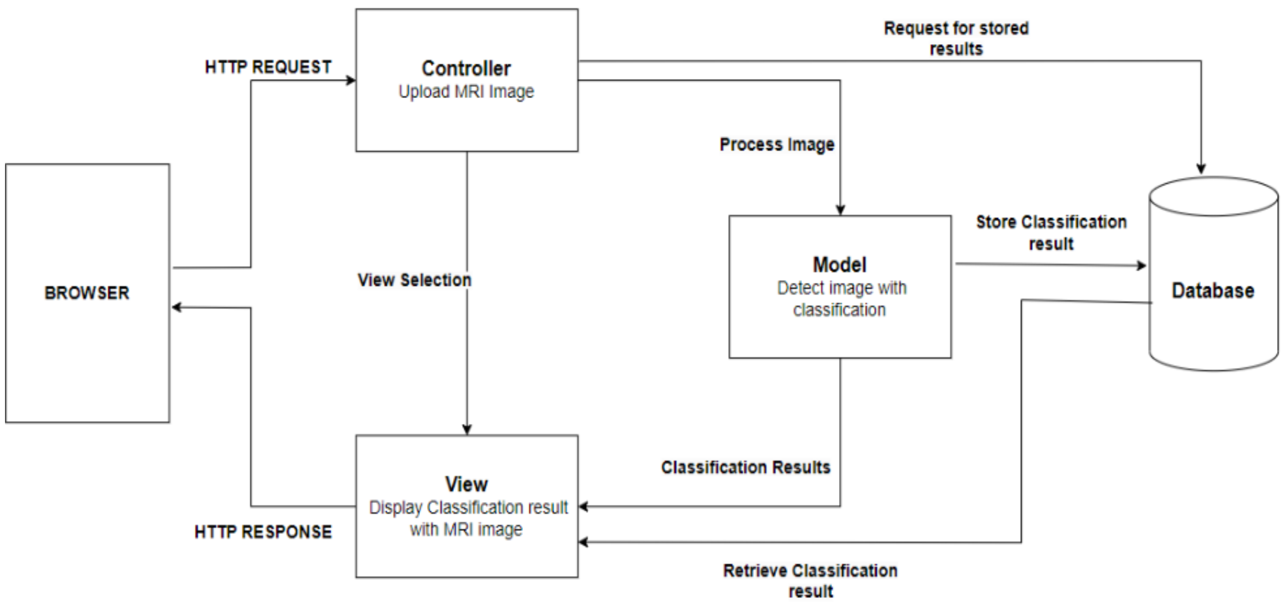

Figure 3.2: MVC Model

MVC separates the system into Model (tumor detection logic), View (user interface), and Controller (user interaction) for clear code organization and easier maintenance. It allows components to be modified or extended independently, making it ideal for evolving medical applications with changing tumor detection algorithms. MVC simplifies testing and debugging efforts. Each component can be tested separately, and changes or issues within one component are confined, making it easier to identify and fix problems. This is particularly important in a medical context where accuracy and reliability are crucial. MVC facilitates parallel development. Different teams or developers can work on the Model, View, and Controller simultaneously without interfering with each other, speeding up the development process. It enables flexible user interface design, accommodating different user needs, devices, and platforms for an optimal user experience.

3.2.2 User Experience(UX) Design

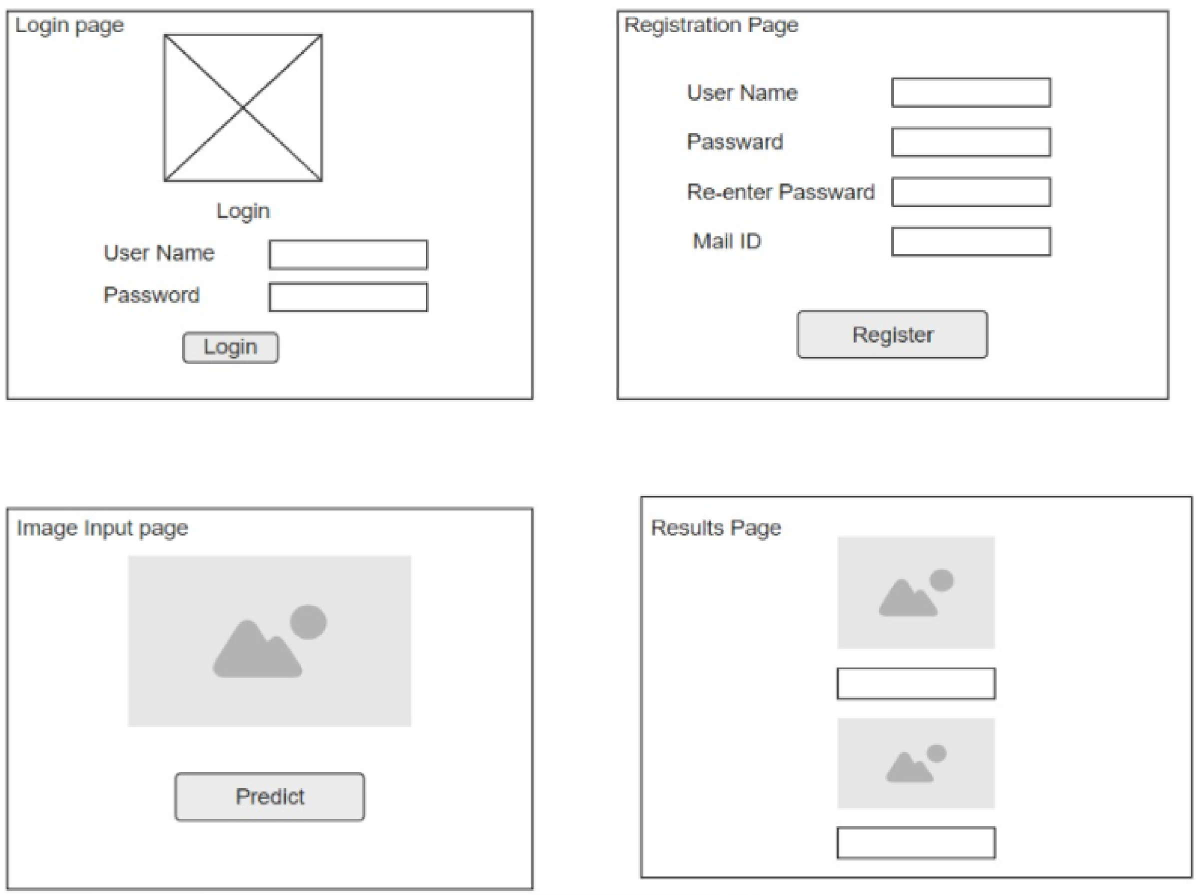

Figure 3.3: User Experience Design

UX design places users at the core of the design process, ensuring that the system is built with a deep understanding of the unique needs and preferences of healthcare professionals. This approach results in a system that aligns with user expectations and workflow, ultimately improving efficiency and user satisfaction. UX design focuses on usability and accessibility, ensuring that the system is easy to use for a wide range of users, including those with varying levels of technical expertise. In a medical setting where time is critical and users may not have extensive training in using the software, a user-friendly interface is paramount. UX design ensures that the interface is intuitive and accessible to all users.

3.3 Dataset Description

3.3.1 Dataset Division:

The dataset, crucial for training and evaluating the model, is divided into three main sets:

- Training Set: This subset of the dataset is used to train the neural network models. The models learn to recognize patterns, features, and representations in the images associated with different classes during the training phase. The larger and more diverse the training set, the better the model can potentially generalize to new, unseen data.
- Test Set: The test set is reserved for evaluating the model's performance after training. It contains images that the model has not seen during the training phase. Assessing the model on the test set helps gauge its ability to generalize to new data and provides insights into its overall performance.
- Validation Set: The validation set is a crucial component for fine-tuning the model during the training process. It helps in preventing overfitting by providing an independent dataset that the model does not use for learning. The performance on the validation set guides decisions regarding model adjustments, such as hyperparameter tuning.

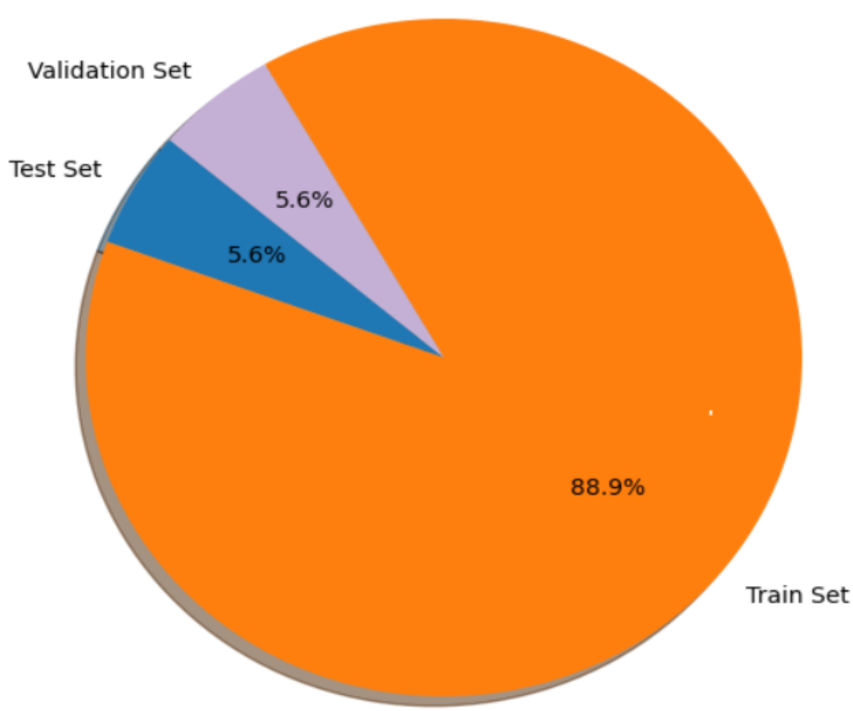

Figure 3.4: Dataset distribution into train, test, and validation set

3.3.2 Classes in the Dataset:

The dataset encompasses four distinct classes:

- Glioma: Images in this class represent cases where brain tumors are classified as Gliomas. Gliomas are a type of tumor that arises from glial cells in the brain.

- Meningioma: Meningiomas are tumors that originate from the meninges, the layers of tissue covering the brain and spinal cord. Images falling into this class pertain to cases with Meningioma tumors.

- Pituitary Tumor: This class comprises images associated with cases where tumors are identified as Pituitary tumors. The pituitary gland, located at the base of the brain, can develop various types of tumors.

- No Tumor: Images in this class represent cases where no brain tumor is detected. This class serves as the baseline for the model to learn what constitutes a 'normal' or 'healthy' image.

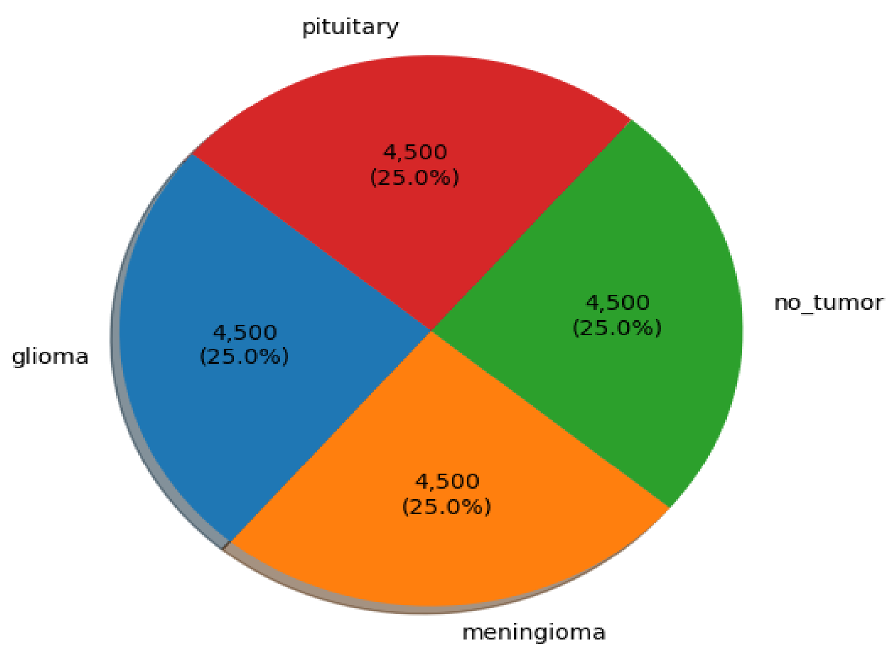

Figure 3.5: Dataset distribution into glioma, meningioma, pituitary and no tumor data set

3.3.3 Augmentation Methods:

Data augmentation is a technique used to artificially expand the training dataset by applying various transformations to the original images. In the context of brain tumor detection, the dataset undergoes augmentation through several methods:

- Random Rotation: Images are randomly rotated by a certain degree during training. This helps the model become robust to variations in tumor orientations.

- Random Flip: Randomly flipping images horizontally or vertically introduces diversity, enabling the model to learn features from different perspectives.

- Random Brightness: Variations in brightness are applied randomly to the images. This helps the model adapt to different lighting conditions that may be encountered in real-world scenarios.

- Adding Noise: Random noise is introduced to the images. This enhances the model's resilience to noisy or less clear images, which can be encountered in medical imaging data sets.

Chapter 4

IMPLEMENTATION

In our study, we looked at six different models— AlexNet, VGG16, ResNet-50, GoogleNet, Xception, and DenseNet-121, to see how well they can detect brain tumors. In the next sections, we'll break down each model to understand how they work and compare their strengths and weaknesses. This detailed analysis helps us figure out which model is best suited for improving brain tumor detection.

4.1 AlexNet

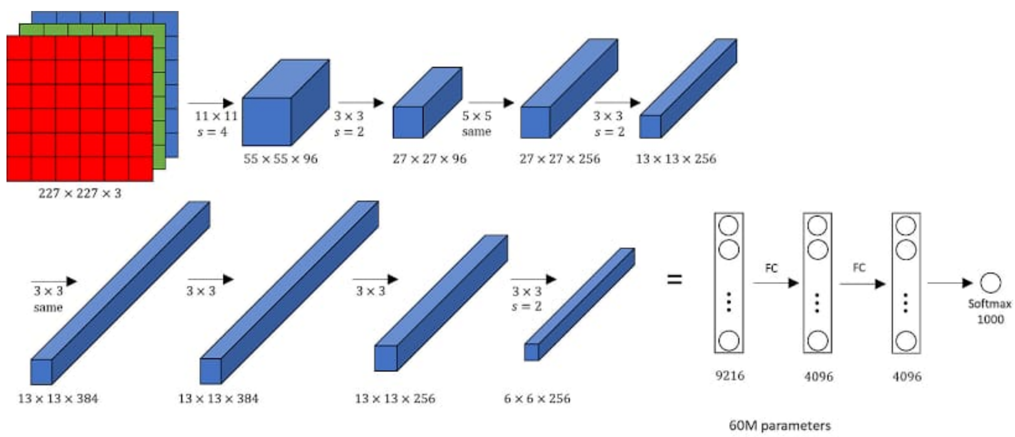

Figure 4.1: Architecture of AlexNet

AlexNet, a groundbreaking convolutional neural network (CNN), achieved unprecedented success in the 2012 ImageNet challenge[9]. Comprising five convolutional layers and three fully connected layers, its design choices, such as ReLU activation, addressed the vanishing gradient problem, enabling effective feature learning. AlexNet introduced max-pooling for spatial downsampling, utilized local response normalization for enhanced generalization, and leveraged GPU acceleration. The architecture's depth and innovative features established a paradigm for subsequent deep learning models.

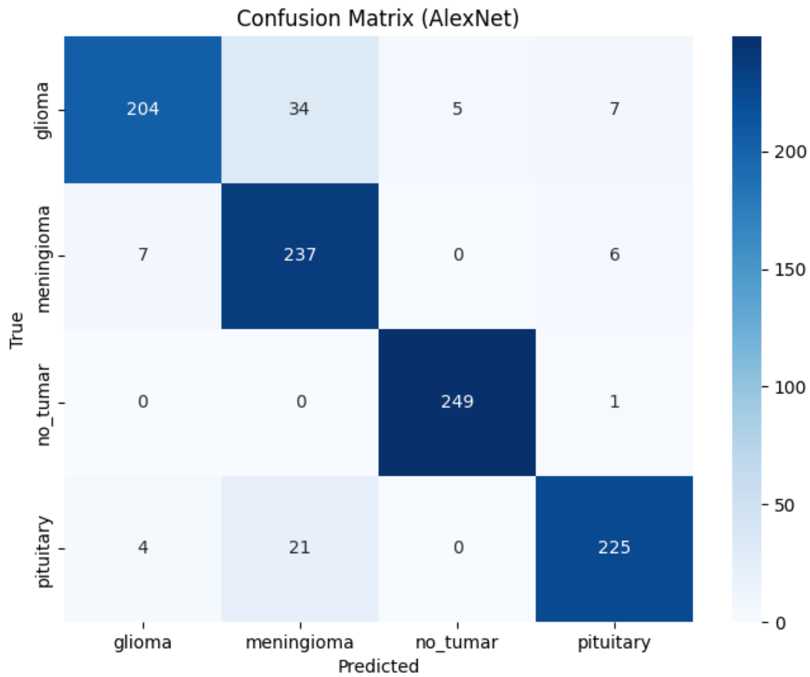

Figure 4.2: Confusion matrix - AlexNet

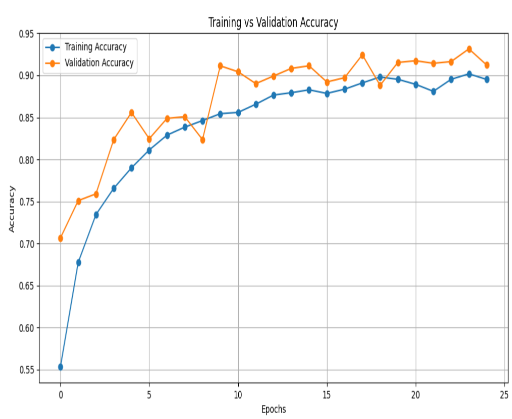

Figure 4.3: Accuracy

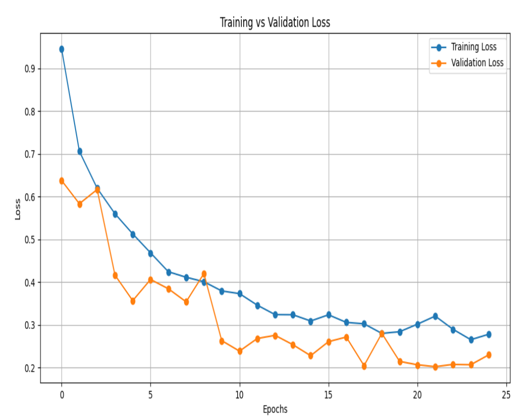

Figure 4.4: Loss

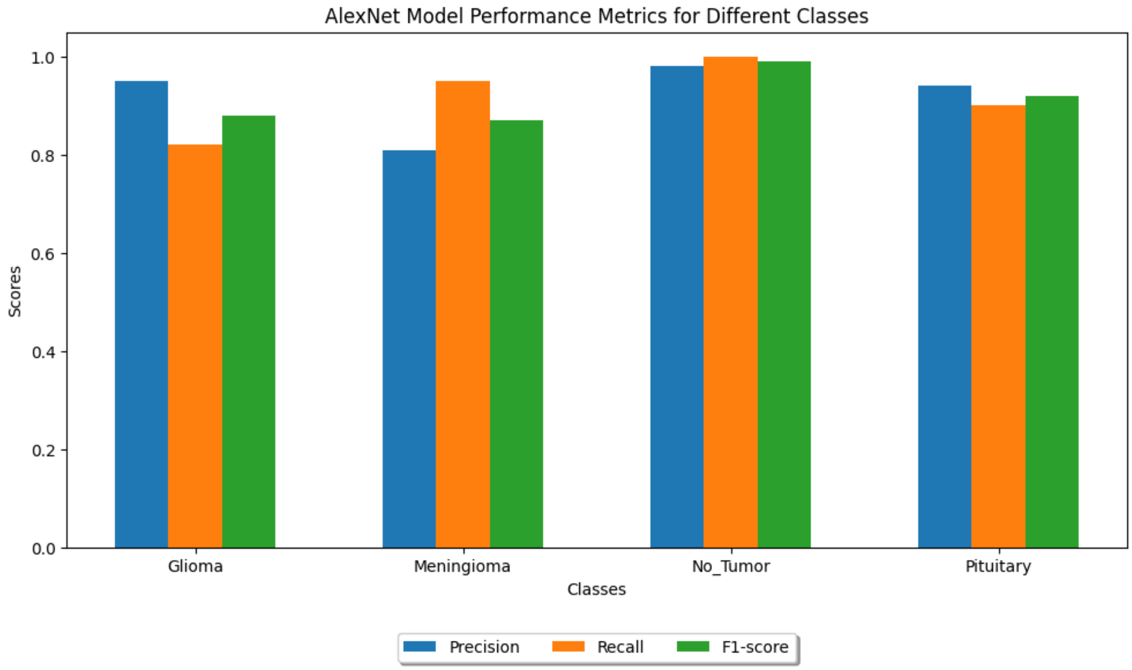

Figure 4.5: AlexNet models precision, recall, f1-score value for each brain tumor class

Table 4.1: AlexNet Model Performance Metrics For Different Class

Classes	**Precision**	**Recall**	**F1-score**	**Support**
Glioma	0.95	0.82	0.88	250
Meningioma	0.81	0.95	0.87	250
No_Tumor	0.98	1.00	0.99	250
Pituitary	0.94	0.90	0.92	250

4.2 VGG16

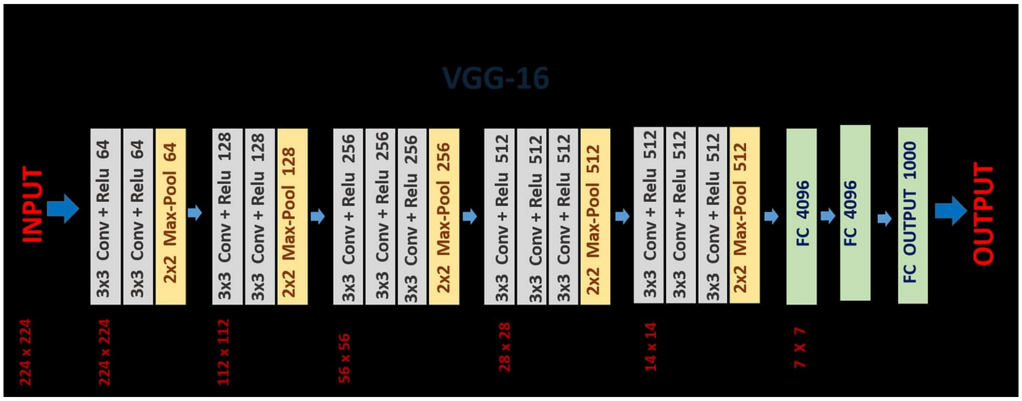

Figure 4.6: Architecture of VGG16

VGG16, developed by the Visual Geometry Group at the University of Oxford, is renowned for its simplicity and effectiveness[10]. Its architecture comprises 16 weight layers, including 13 convolutional layers and three fully connected layers. Notably, VGG16 employs small-sized (3x3) convolutional filters throughout the network, contributing to a uniform structure. The consistent use of these filters aids in capturing intricate features at different spatial scales. The architecture's straightforward design makes it easy to understand and implement. Each convolutional block is followed by max-pooling, leading to a progressive reduction in spatial dimensions. The fully connected layers at the end enable high-level feature extraction and classification. VGG16's uniformity facilitates its transferability to various image classification tasks.

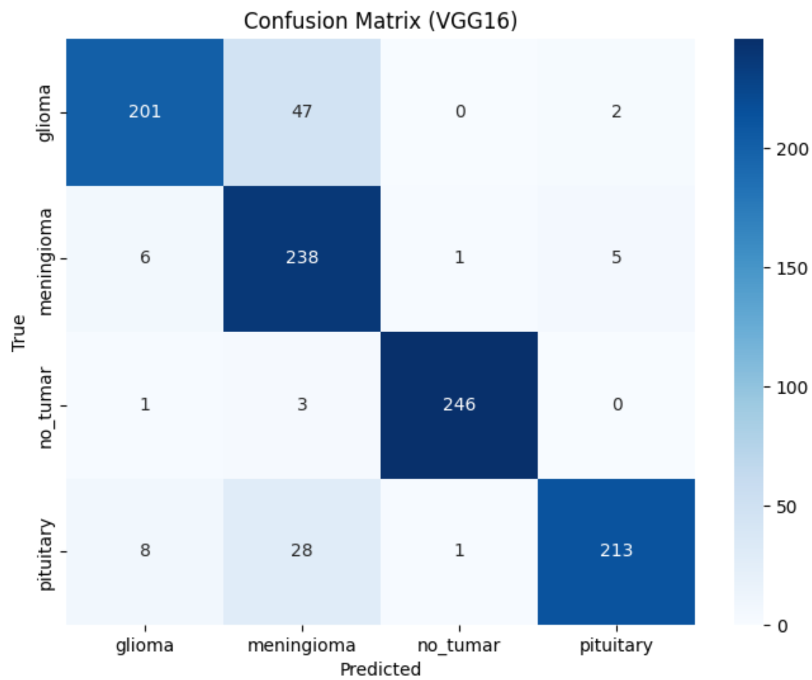

Figure 4.7: Confusion matrix - VGG16

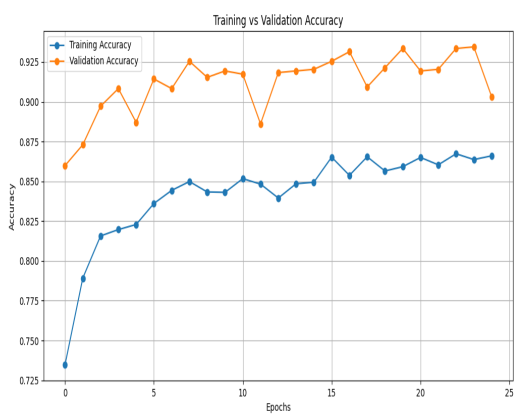

Figure 4.8: Accuracy

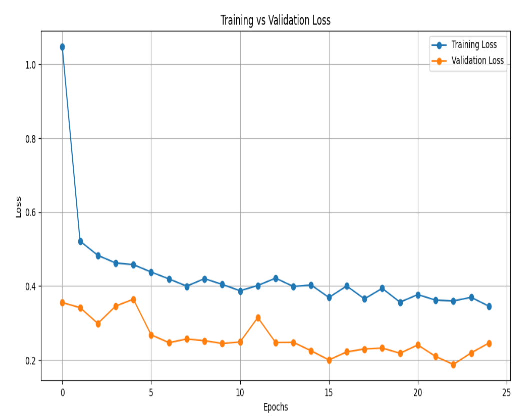

Figure 4.9: Loss

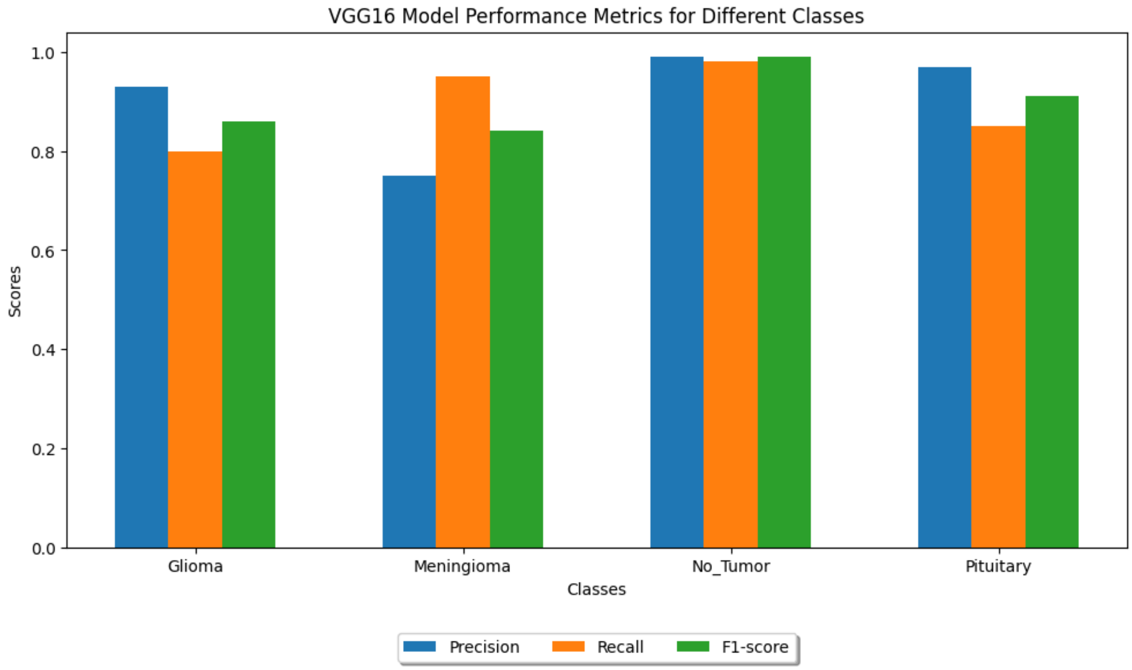

Figure 4.10: VGG16 models precision, recall, f1-score value for each brain tumor class

Table 4.2: VGG16 Model Performance Metrics For Different Class

Classes	**Precision**	**Recall**	**F1-score**	**Support**
Glioma	0.93	0.80	0.86	250
Meningioma	0.75	0.95	0.84	250
No_Tumor	0.99	0.98	0.99	250
Pituitary	0.97	0.85	0.91	250

4.3 ResNet-50

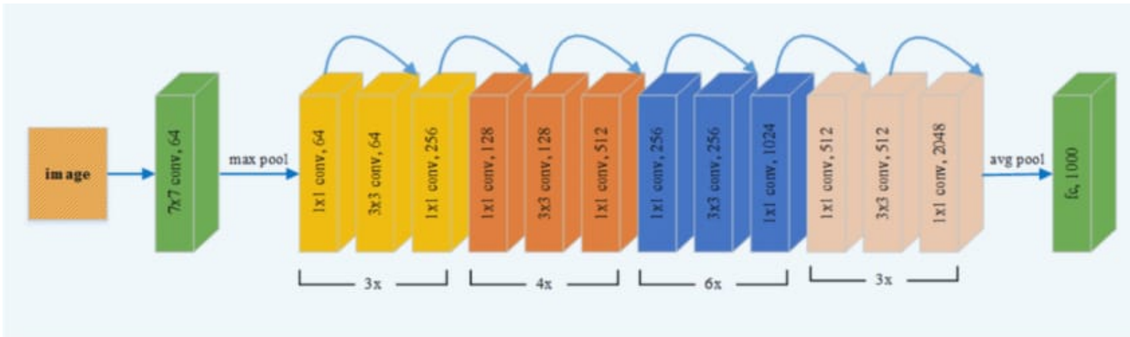

Figure 4.11: Architecture of ResNet-50

ResNet50, part of the Residual Network (ResNet) family, introduced a revolutionary concept called residual learning. Proposed by Kaiming He et al. in 2015 [11], ResNet50 addresses the challenge of training very deep networks. Its architecture includes shortcut connections that allow the network to bypass certain layers during training, mitigating the vanishing gradient problem. With 50 weight layers, including residual blocks, ResNet50 excels in capturing intricate patterns and features in images. The residual connections facilitate the training of deep networks by enabling the direct flow of gradients. The architecture's success lies in its ability to capture both low and high-level features efficiently. The skip connections allow for the preservation of information throughout the network, making ResNet50 highly effective in image recognition and object detection tasks.

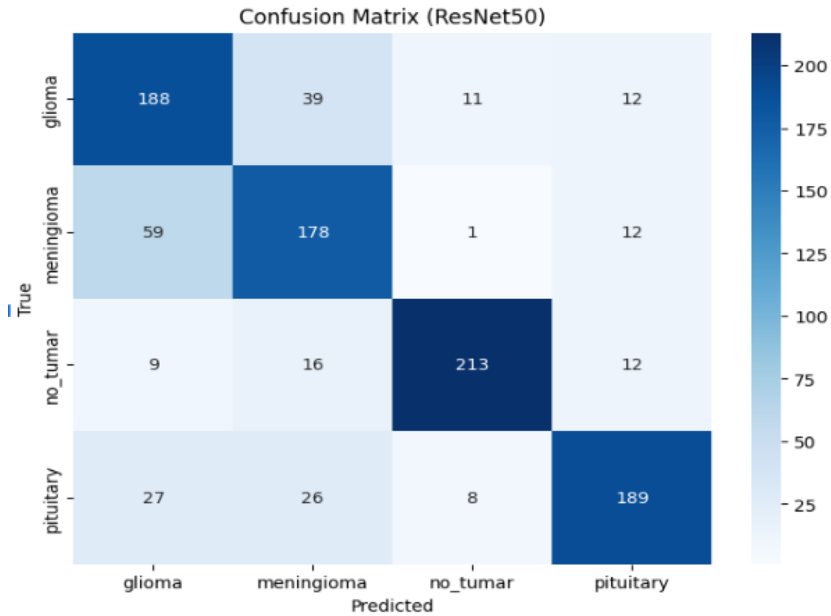

Figure 4.12: Confusion matrix - ResNet

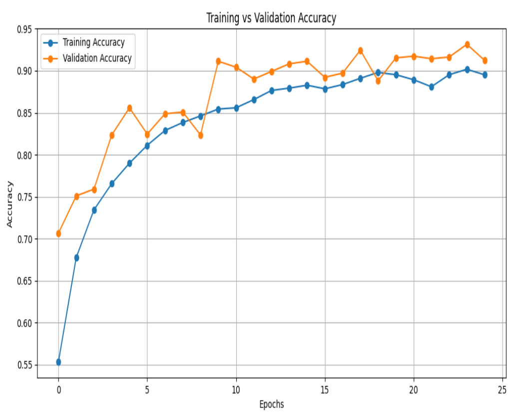

Figure 4.13: Accuracy

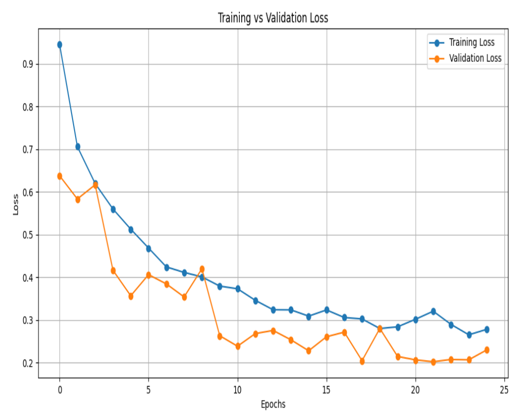

Figure 4.14: Loss

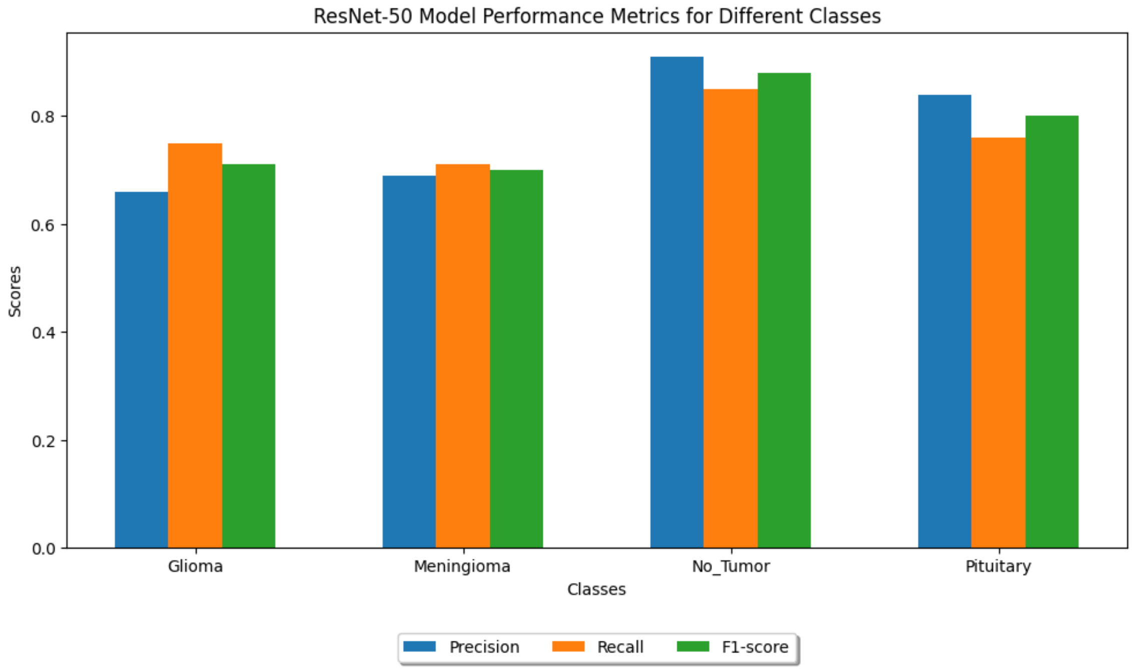

Figure 4.15: ResNet-50 models precision, recall, f1-score value for each brain tumor class

Table 4.3: ResNet-50 Model Performance Metrics For Different Class

Classes	**Precision**	**Recall**	**F1-score**	**Support**
Glioma	0.66	0.75	0.71	250
Meningioma	0.69	0.71	0.70	250
No_Tumor	0.91	0.85	0.88	250
Pituitary	0.84	0.76	0.80	250

4.4 GoogleNet

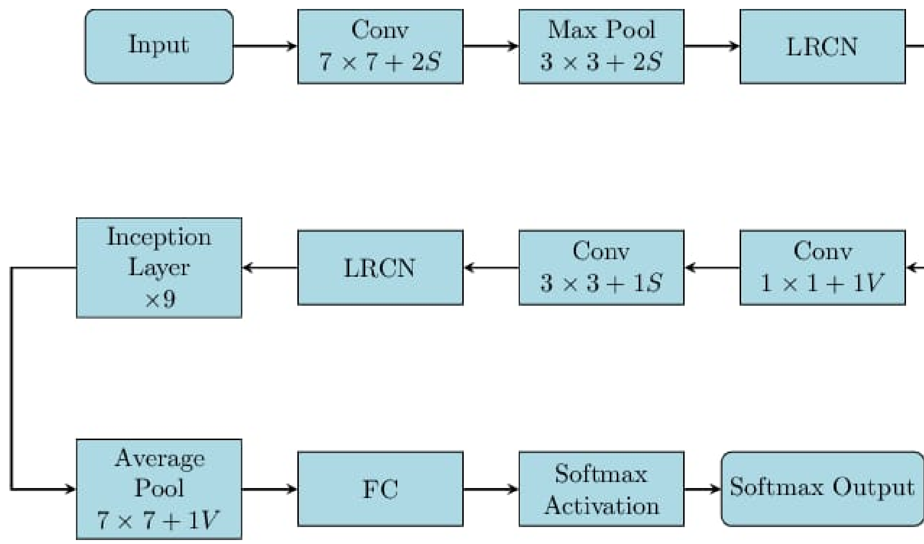

Figure 4.16: Architecture of GoogleNet

GoogleNet, or Inception V1 [12], was introduced by Google researchers in 2014. What sets GoogleNet apart is its innovative inception modules, which employ filters of multiple sizes concurrently. This enables the network to capture features at different spatial scales, enhancing its ability to recognize complex patterns in images. The architecture's inception modules are designed to extract features of varying complexities efficiently. Notably, GoogleNet introduces 1x1 convolutions for dimensionality reduction, allowing for more efficient use of computational resources. The incorporation of multiple parallel convolutional paths within each inception module enhances the network's representational power. GoogleNet's emphasis on computational efficiency, thanks to its inception modules, makes it well-suited for tasks demanding intricate feature extraction, such as image classification.

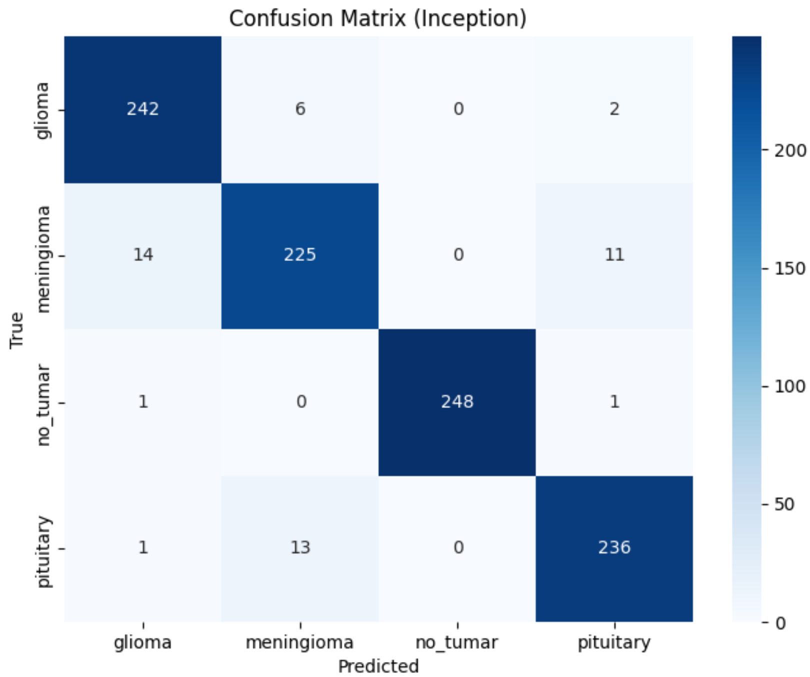

Figure 4.17: Confusion matrix - GoogleNet

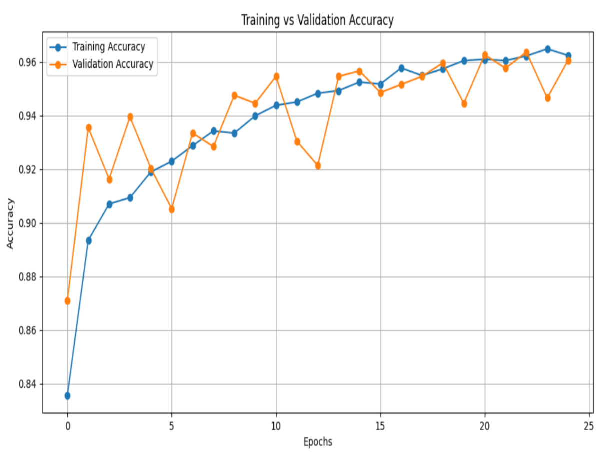

Figure 4.18: Accuracy

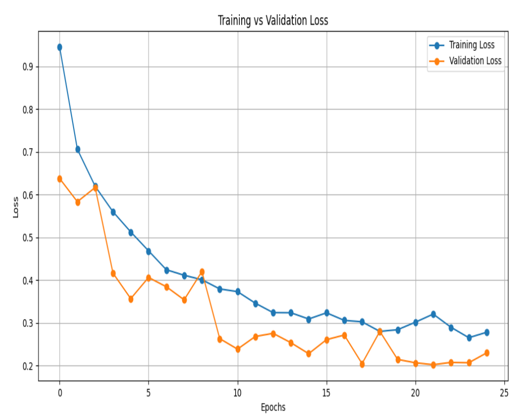

Figure 4.19: Loss

Figure 4.20: GoogleNet models precision, recall, f1-score value for each brain tumor class

Table 4.4: GoogleNet Model Performance Metrics For Different Class

Classes	**Precision**	**Recall**	**F1-score**	**Support**
Glioma	0.94	0.97	0.95	250
Meningioma	0.92	0.90	0.91	250
No_Tumor	1.00	0.99	1.00	250
Pituitary	0.94	0.94	0.94	250

4.5 Xception

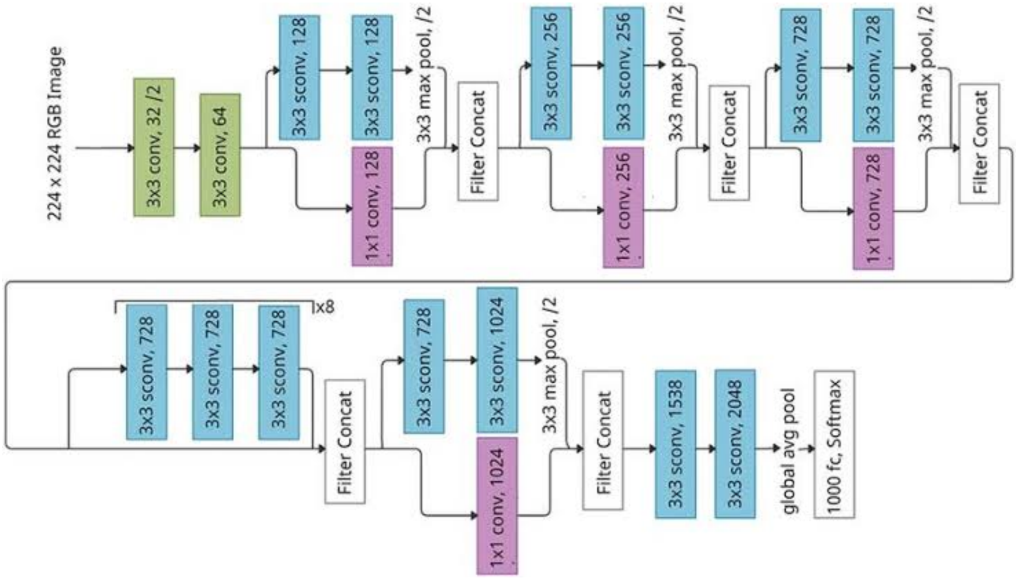

Figure 4.21: Architecture of Xception

Xception, short for "Extreme Inception," represents an evolution of the Inception architecture. François Chollet, the man of the Keras library, proposed Xception [13], which uses depthwise separable convolutions in place of the conventional inception modules. This modification enhances the model's parameter efficiency and computational power. Depthwise separable convolutions decouple spatial and channel-wise convolutions, reducing the number of parameters and computation required. Xception excels in feature extraction tasks, making it a powerful choice for image classification, especially when computational resources are a consideration. The architecture's depthwise separable convolutions allow it to capture complex features while maintaining computational efficiency. Xception's design principles make it well-suited for applications where both accuracy and resource efficiency are critical.

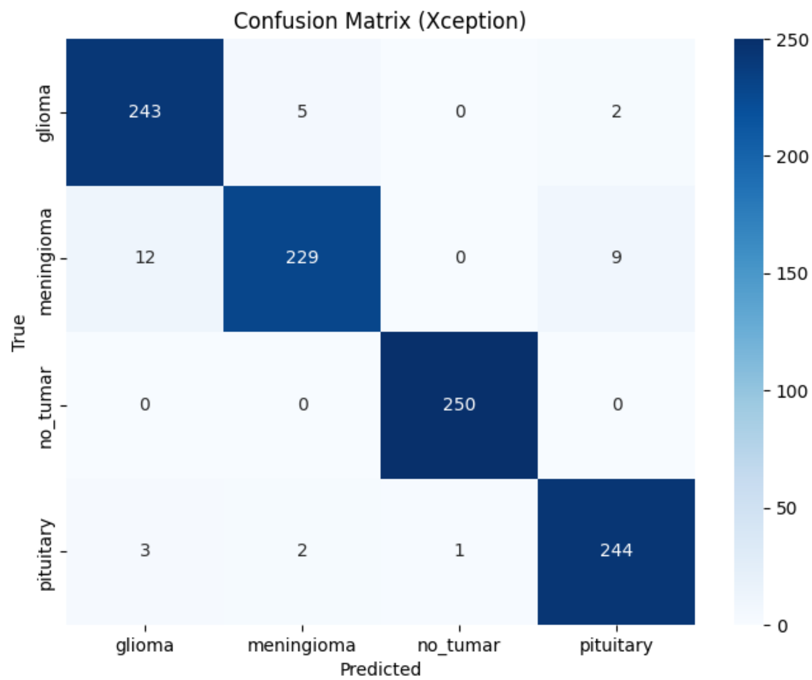

Figure 4.22: Confusion matrix - Xception

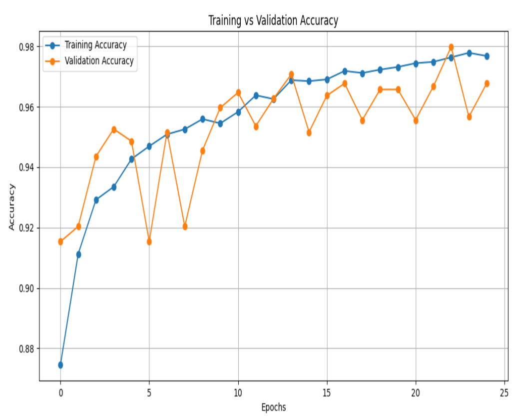

Figure 4.23: Accuracy

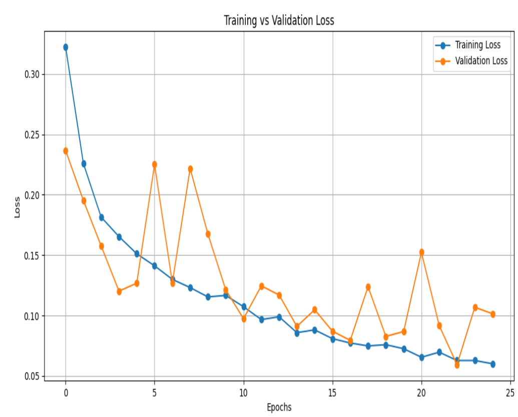

Figure 4.24: Loss

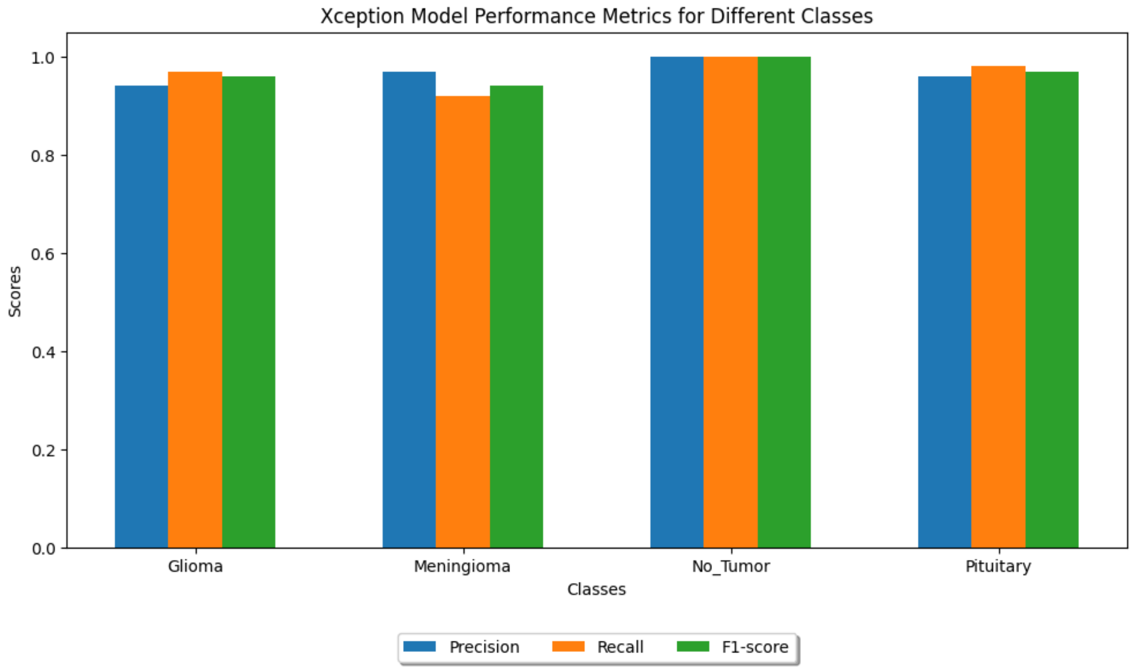

Figure 4.25: Xception models precision, recall, f1-score value for each brain tumor class

Table 4.5: Xception Model Performance Metrics For Different Class

Classes	**Precision**	**Recall**	**F1-score**	**Support**
Glioma	0.94	0.97	0.96	250
Meningioma	0.97	0.92	0.94	250
No_Tumor	1.00	1.00	1.00	250
Pituitary	0.96	0.98	0.97	250

4.6 DenseNet-121

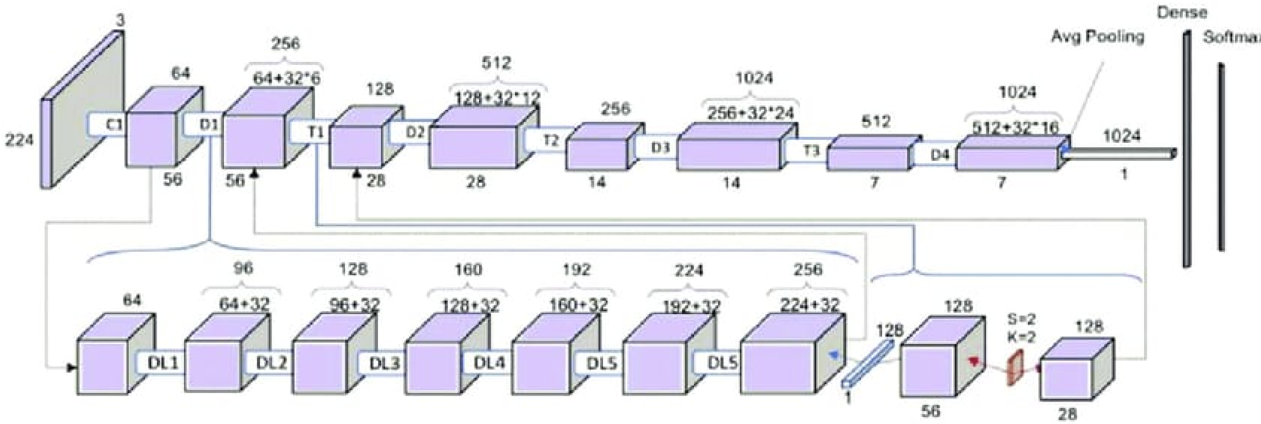

Figure 4.26: Architecture of DenseNet-121

DenseNet121, part of the DenseNet (Densely Connected Convolutional Network) series, introduced a novel concept called dense connectivity. Developed by Gao Huang et al. in 2016 [14], DenseNet architectures foster dense connections between layers, where each layer receives direct inputs from all preceding layers. This dense connectivity facilitates feature reuse, reduces the vanishing gradient problem, and encourages efficient learning of intricate patterns. DenseNet121, specifically, has 121 layers and has demonstrated success in various image classification tasks. The architecture's parameter efficiency, thanks to feature reuse, and its ability to capture fine-grained details make it a compelling choice for tasks demanding a comprehensive understanding of visual data. In DenseNet121, each layer receives the feature maps of all preceding layers as input, leading to dense connections. This architecture promotes feature reuse, as each layer has access to the features extracted by all preceding layers. Additionally, DenseNet121 addresses the vanishing gradient problem by facilitating direct gradient flow through the densely connected layers. The dense connectivity results in models that are more parameter-efficient and computationally powerful, contributing to their success in image classification tasks.

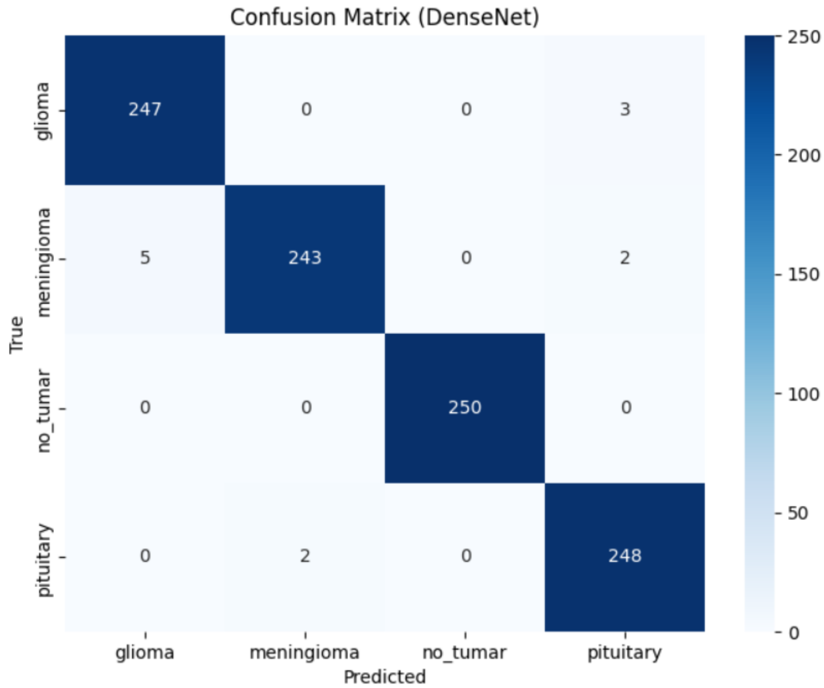

Figure 4.27: Confusion matrix - DenseNet

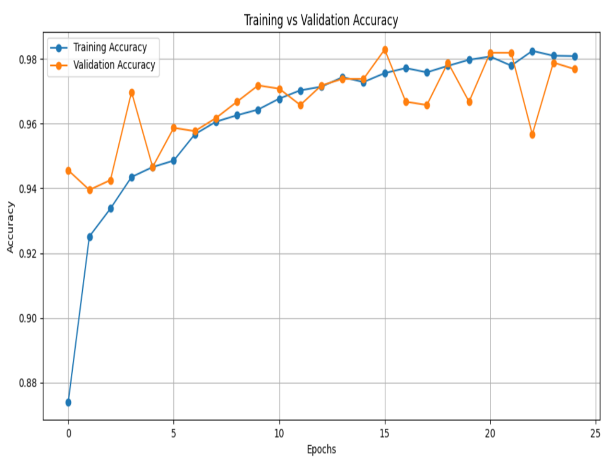

Figure 4.28: Accuracy

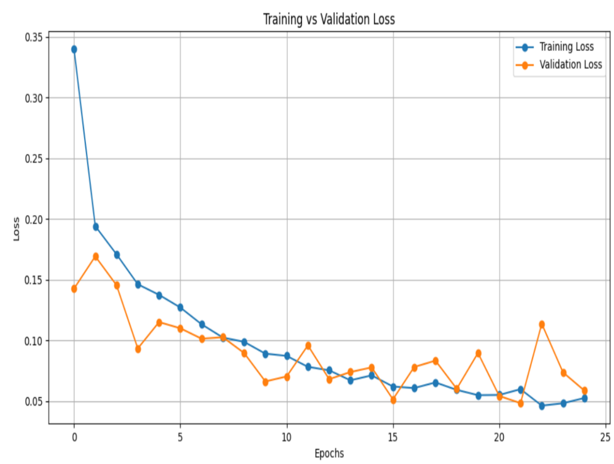

Figure 4.29: Loss

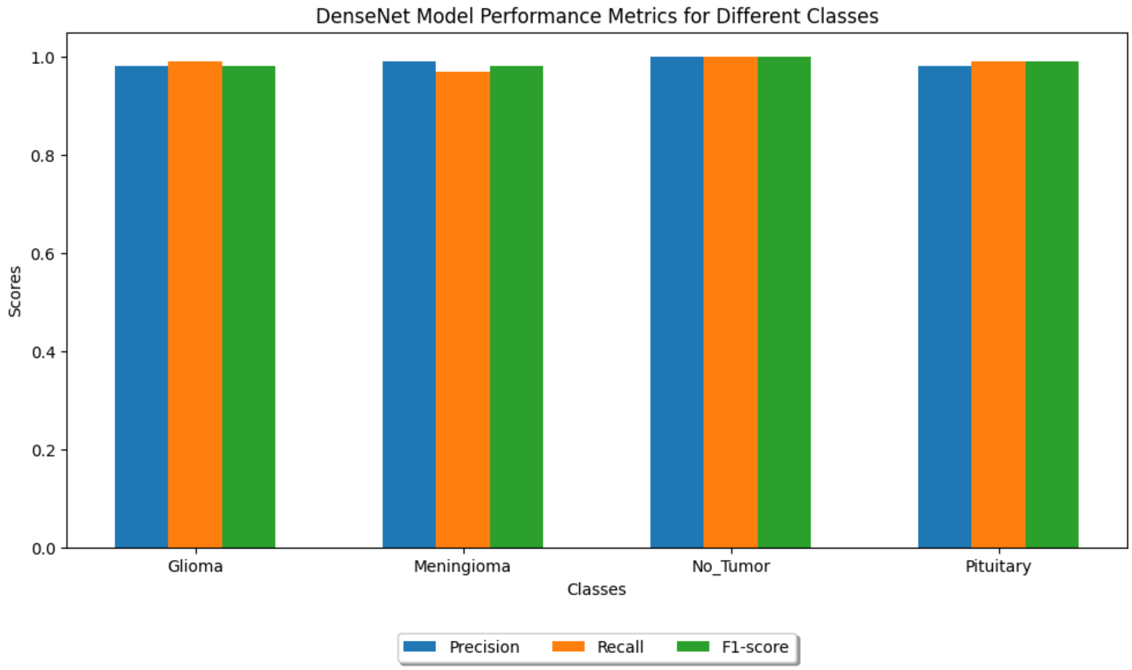

Figure 4.30: DenseNet-121 models precision, recall, f1-score value for each brain tumor class

Table 4.6: DenseNet-121 Model Performance Metrics For Different Class

Classes	**Precision**	**Recall**	**F1-score**	**Support**
Glioma	0.98	0.99	0.98	250
Meningioma	0.99	0.97	0.98	250
No_Tumor	1.00	1.00	1.00	250
Pituitary	0.98	0.99	0.99	250

4.7 Evaluation Metrics

The evaluation metrics, including training accuracy, testing accuracy, validation accuracy, precision, recall, and F1 score, follow the same formulas for all six models. These metrics provide a standardized and consistent way to assess the performance of each model in brain tumor detection, ensuring a comprehensive and comparable evaluation across the diverse architectures employed in the study.

- **Training Accuracy:**

$$\text{Training Accuracy} = \frac{\text{Number of Correct Predictions in Training}}{\text{Total Number of Instances in Training}}$$

  - Measures the proportion of correct predictions made by the model on the training dataset.
  - Assesses how well the model fits the training data.

- **Testing Accuracy:**

$$\text{Testing Accuracy} = \frac{\text{Number of Correct Predictions in Testing}}{\text{Total Number of Instances in Testing}}$$

  - Measures the proportion of correct predictions made by the model on a separate testing dataset that it hasn't seen during training.
  - Indicates how well the model generalizes to new, unseen data.

- **Validation Accuracy:**

$$\text{Validation Accuracy} = \frac{\text{Number of Correct Predictions in Validation}}{\text{Total Number of Instances in Validation}}$$

  - Measures the proportion of correct predictions made by the model on a validation dataset, typically used for tuning model hyperparameters.
  - Helps prevent overfitting by assessing the model's performance on a dataset that is not used for training.

- **Precision:**

$$\text{Precision} = \frac{\text{TP}}{\text{TP} + \text{FP}}$$

  - Precision measures how well the model predicts the favourable outcomes.
  - This is the proportion of actual positive predictions to all of the model's positive predictions.
  - Low false positive rate is indicated by high precision.

- **Recall Formula:**

$$\text{Recall} = \frac{\text{True Positives}}{\text{True Positives} + \text{False Negatives}}$$

  - Recall, which is sometimes referred to as sensitivity or true positive rate, assesses how well the model can locate all pertinent instances within the dataset.
  - It is the proportion of all actual positive occurrences to all true positive expectations.
  - Low false negative rates are indicated by high recall.

- **F1 Score Formula:**

$$\text{F1 Score} = \frac{2 \cdot (\text{Precision} \cdot \text{Recall})}{\text{Precision} + \text{Recall}}$$

  - The F1 Score is a single statistic that takes into account both false positives and false negatives. It is calculated as the harmonic mean of precision and recall.
  - Beneficial in cases where class disparities exist.

Chapter 5

RESULTS AND DISCUSSIONS

Below is the result analysis of the models we used for this project. We used six different models and compared their Training Accuracy, Validation Accuracy, Test Accuracy, Training loss, Validation Loss and Total training time.

Table 5.1: Performance Metrics of Different Models

Model	**Train Acc (%)**	**Val Acc (%)**	**Test Acc (%)**	**Train Loss (%)**	**Val Loss (%)**	**Time (s)**
AlexNet	90	91	89.8	28	24	5729.75
VGG16	87.5	90	90.1	37	23.8	4983.86
ResNet-50	76	78	75.19	58	52	6051.01
GoogleNet	98	97	94.9	10	12.9	5645.39
Xception	97.8	96.8	98	7	10	5462.67
DenseNet-121	98.1	97.8	98.1	6	7	5833.79

According to above Table DenseNet-121 gives highest Test accuracy and less loss comapred to other models. DenseNet 121 stands out among the six models, namely VGG16, ResNet-50, Xception, GoogleNet, AlexNet, and itself, due to its characteristic properties that contribute to superior accuracy. The architecture's dense connectivity, where each layer is connected to every other layer, promotes efficient feature reuse and gradient flow, addressing challenges like the vanishing gradient problem. This results in parameter efficiency and enables the network to capture intricate patterns through hierarchical feature learning. The ensemble effect, facilitated by dense connectivity, enhances the model's ability to discriminate between classes. Moreover, DenseNet's emphasis on spatial and channel feature interactions, along with its adaptive growth parameter, further contributes to its effectiveness in image classification tasks. The combination of these properties establishes DenseNet 121 as a powerful model for extracting and leveraging complex features, leading to its highest accuracy among the evaluated models.

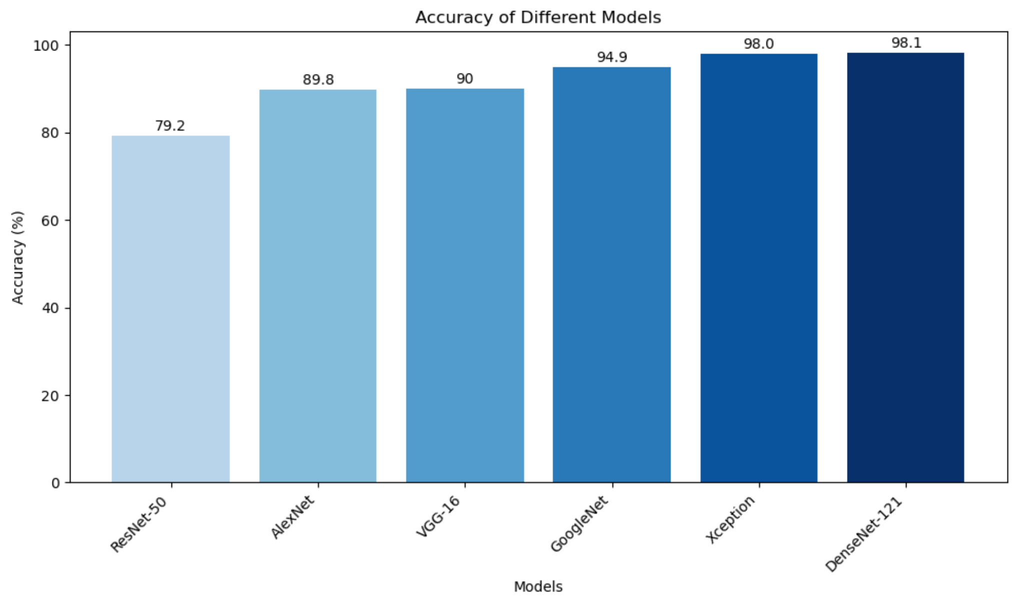

Figure 5.1: Test accuracy of different models

5.1 User Interface

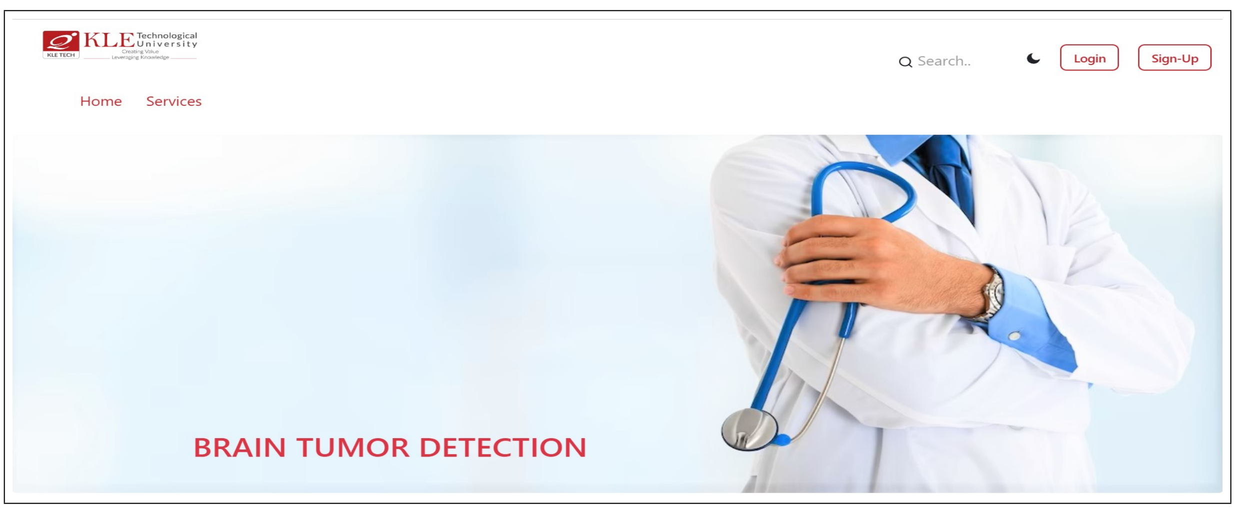

Figure 5.2: Home Page

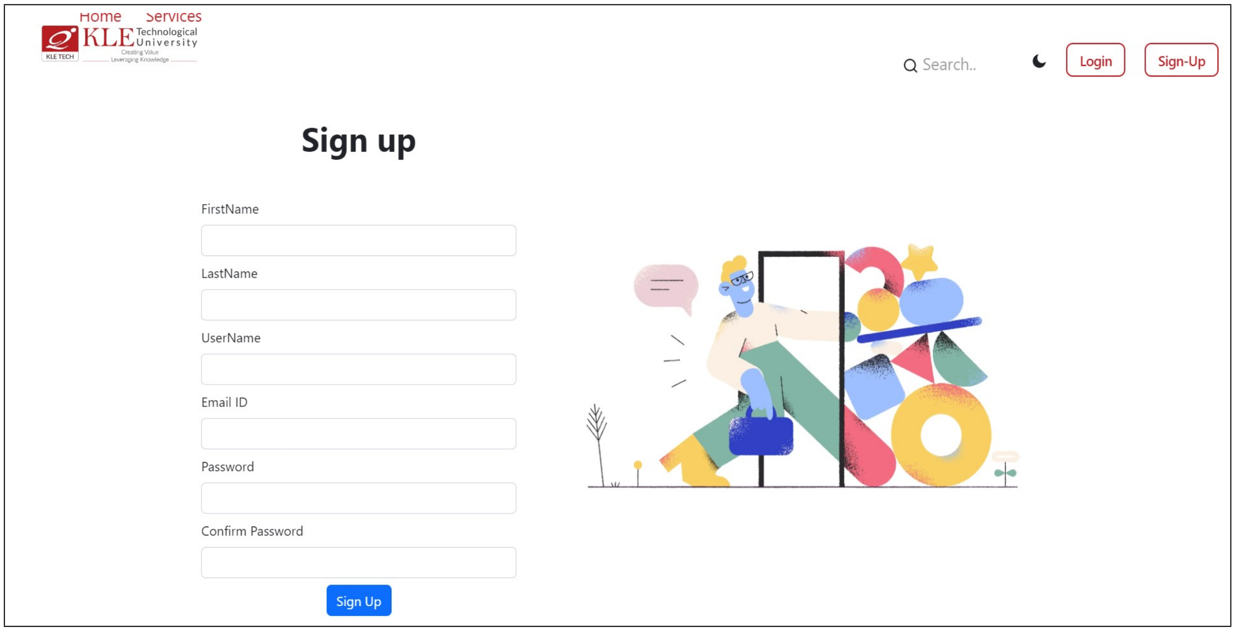

Figure 5.3: Signup Page

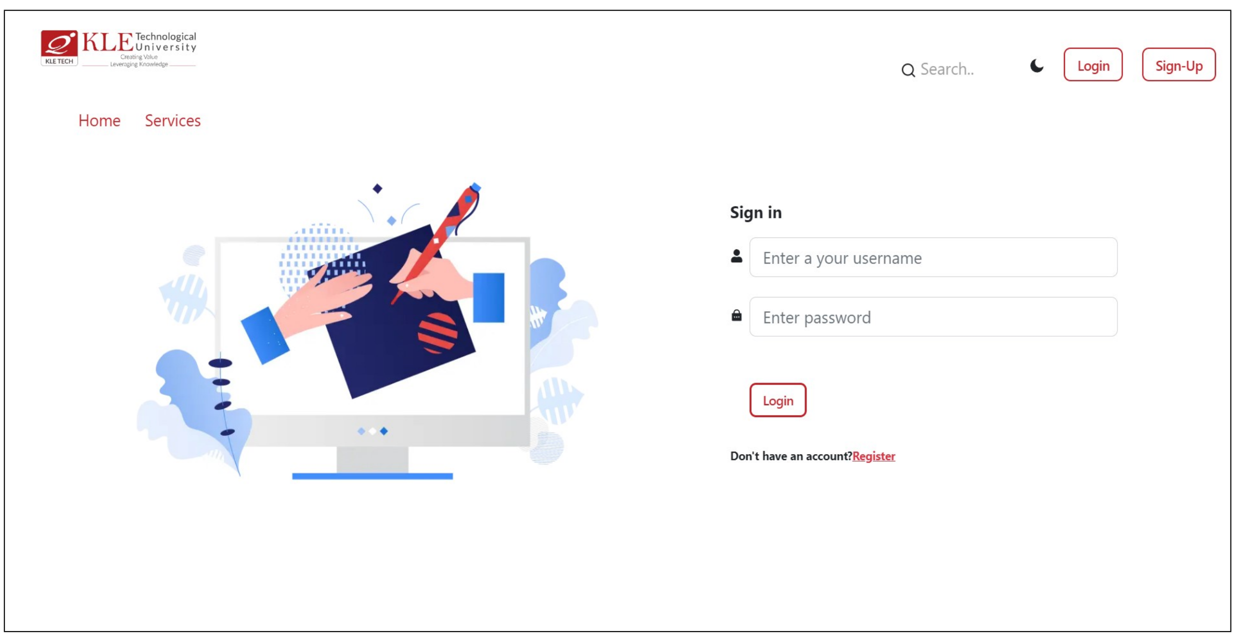

Figure 5.4: Login Page

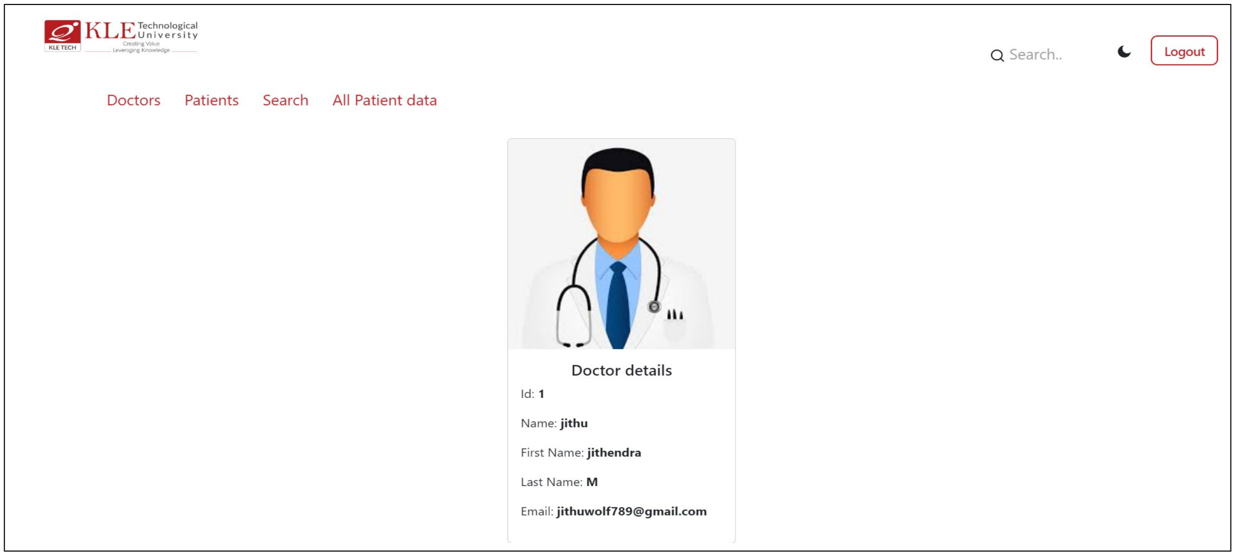

Figure 5.5: Doctor Details

Figure 5.6: Patient details form page

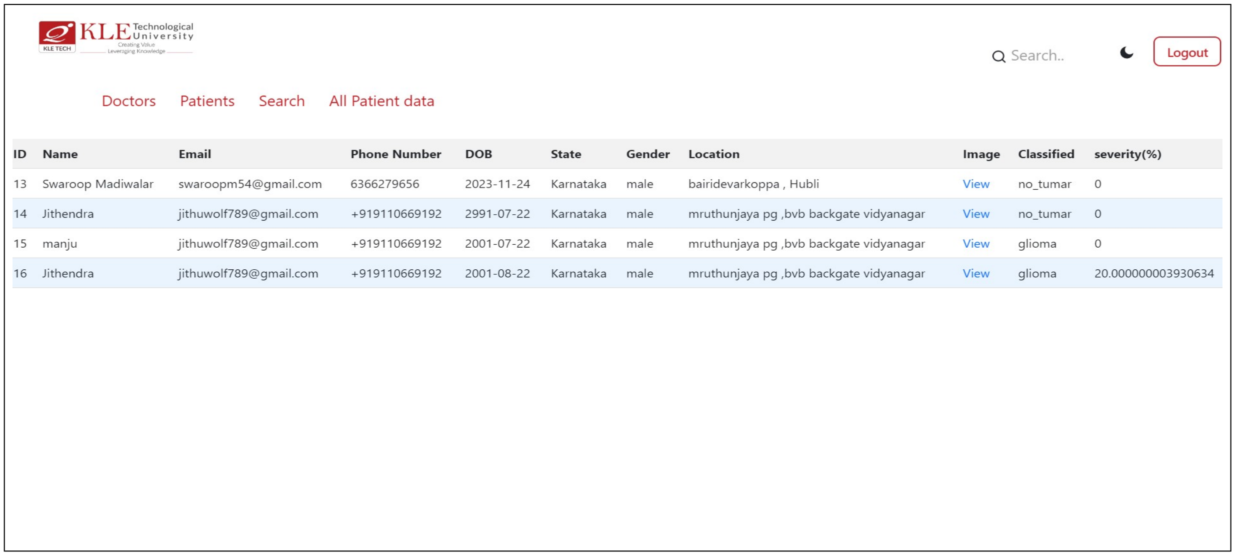

Figure 5.7: Result Page

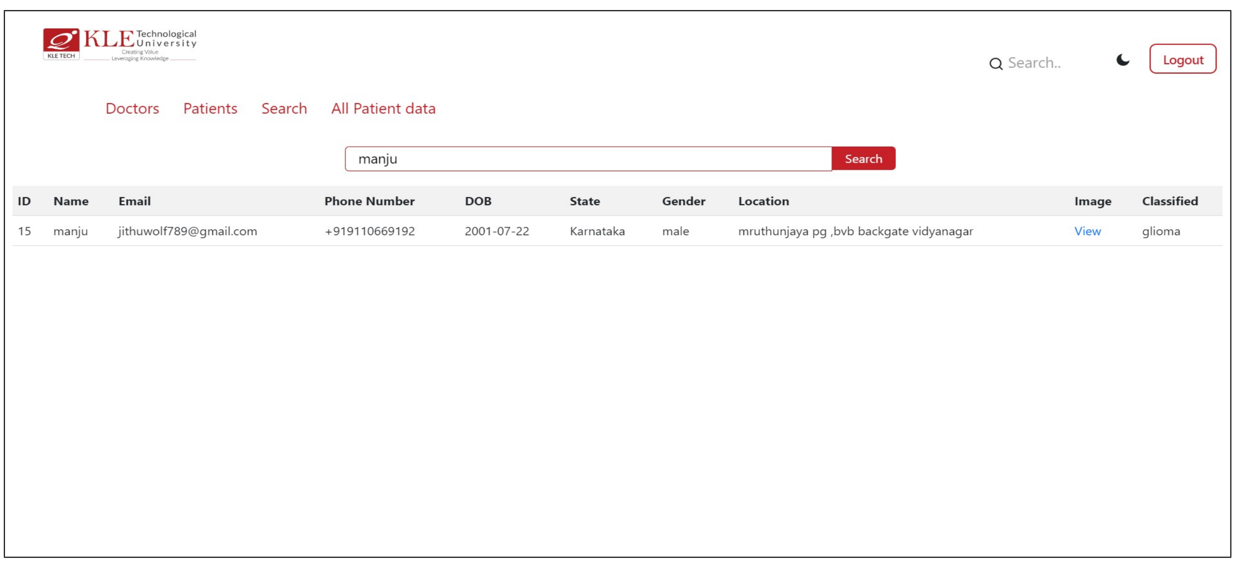

Figure 5.8: Search Page

Chapter 6

CONCLUSION AND FUTURE SCOPE OF THE WORK

In the brain tumor detection and classification system, six distinct models—AlexNet, ResNet-50, Xception, Inception, DenseNet-121, and VGG16—were employed. Following a thorough evaluation, DenseNet-121 emerged as the most effective, demonstrating superior accuracy in classifying brain MRI images into glioma, meningioma, pituitary tumor, and no tumor. This remarkable performance underscores the robustness and effectiveness of DenseNet architecture tailored for the specific task.

Looking ahead, future enhancements could encompass extending the classification to include other types of brain tumors. Future work may extend the brain tumor system by exploring tumor stages over time. This temporal analysis could enhance diagnostic precision, guide personalized treatments, and require advanced deep learning architectures to capture evolving patterns in medical imaging data.

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